

- 1 -

## SEQUENCE LISTING

&lt;110&gt; Bayer AG, BHC

&lt;120&gt; Diagnostics and Therapeutics for Diseases Associated with HM74 (HM74)

&lt;130&gt; Le A 36 590

&lt;160&gt; 5

&lt;170&gt; PatentIn version 3.1

&lt;210&gt; 1

&lt;211&gt; 2051

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 1

```

cgccactttg ctggagcatt cactagggcga ggcgctccat cggactcact agccgcactc      60
atgaatcggc accatctgca ggatcacttt ctggaaatag acaagaagaa ctgctgtgtg      120
ttccgagatg acttcattgc caaggtgttg ccgcccgtgt tggggctgga gtttatcttt      180
gggcttcttg gcaatggcct tgccctgtgg attttctgtt tccacctcaa gtcctggaaa      240
tccagccgga ttttctgtt caacctggca gtagctgact ttctactgat catctgcctg      300
ccgttcgtga tggactacta tgtgcggcgt tcagactgga actttgggga catcccttgc      360
cggctgggtg tcttcattgt tgccatgaac cgccagggca gcatcatctt cctcacgggtg      420
gtggcggtag acaggtatct cccgggtggt catccccacc acgccttgaa caagatctcc      480
aattggacag cagccatcat ctcttgccct ctgtggggca tccactgttg cctaacagtc      540
cacctcctga agaagaagtt gctgatccag aatggccctg caaatgtgtg catcagcttc      600
agcatctgcc ataccttccg gtggcacgaa gctatgttcc tccctggagt cctcctgccc      660
ctgggcatca tcctgttctg ctcagccaga attatctgga gcctgcggca gagacaaatg      720
gacccggcatg ccaagatcaa gagagccatc accttcatca tgggtggtgg catcgtcttt      780
gtcatctgct tccttcccag cgtggttgtg cggatccgca tcttctggct cctgcacact      840
tcgggcacgc agaattgtga agtgtaccgc tcggtggacc tggcgttctt tatcactctc      900
agcttcacct acatgaacag catgctggac cccgtgggtg actacttctc cagcccatcc      960
tttcccaact tcttctccac tttgatcaac cgctgcctcc agaggaagat gacaggtgag      1020
ccagataata accgcagcac gagcgctcgag ctacacaggg accccaacaa aaccagaggc      1080
gctccagagg cgttaatggc caactccggt gagccatgga gccctcttta tctgggcccc      1140
acctcaaata accattccaa gaagggacat tgtcaccaag aaccagcatc tctggagaaa      1200
cagttgggct gttgcatcga gtaatgtcac tggactcggc ctaagggttc ctggaacttc      1260
cagattcaga gaatctgatt tagggaaact gtggcagatg agtgggagac tgggtgcaag      1320
gtgtgaccac aggaatcctg gaggaacaga gagttaaagct tctaggcatc tgaaacttgc      1380
ttcatctctg acgctcgag gactgaagat gggcaaattg taggcgtttc tgctgagcag      1440
agttggagcc agagatctac ttgtgacttg ttggccttct tccacatct gcctcagact      1500
ggggggggct cagctcctcg ggtgatatct agcctgcttg tgagctctag cagggataag      1560
gagagctgag attggagggg attgtgttgc tcctggagga agcccaggca tcattaaaca      1620
agccagtagg tcacctggct tccgtggacc aattcatctt tcagacaagc tttagagaaa      1680
tggactcagg gaagagactc acatgctttg gttagtatct gtgtttccgg tgggtgtaat      1740
aggggattag cccagaagg gactgagcta aacagtgtta ttatgggaaa ggaaatggca      1800
ttgctgcttt caaccagcga ctaatgcaat ccattcctct cttgtttata gtaatctaag      1860
ggttgagcag ttaaaacggc ttcaggatag aaagctgttt cccacctgtt tcggtttacc      1920
attaaaaggg aaacgtgcct ctgccccacg ggtagagggg gtgcacgttc ctctgggttc      1980
cttcgcttgt gtttctgtac ttacaaaaaa tctaccactt caataaattt tgataggaga      2040
caaaaaaaaaa a

```

&lt;210&gt; 2

&lt;211&gt; 387

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 2

```

Met Asn Arg His His Leu Gln Asp His Phe Leu Glu Ile Asp Lys Lys
1          5          10          15
Asn Cys Cys Val Phe Arg Asp Asp Phe Ile Ala Lys Val Leu Pro Pro
20          25          30
Val Leu Gly Leu Glu Phe Ile Phe Gly Leu Leu Gly Asn Gly Leu Ala
35          40          45

```

- 2 -

Leu Trp Ile Phe Cys Phe His Leu Lys Ser Trp Lys Ser Ser Arg Ile  
 50 55 60  
 Phe Leu Phe Asn Leu Ala Val Ala Asp Phe Leu Leu Ile Ile Cys Leu  
 65 70 75 80  
 Pro Phe Val Met Asp Tyr Tyr Val Arg Arg Ser Asp Trp Asn Phe Gly  
 85 90 95  
 Asp Ile Pro Cys Arg Leu Val Leu Phe Met Phe Ala Met Asn Arg Gln  
 100 105 110  
 Gly Ser Ile Ile Phe Leu Thr Val Val Ala Val Asp Arg Tyr Phe Arg  
 115 120 125  
 Val Val His Pro His His Ala Leu Asn Lys Ile Ser Asn Trp Thr Ala  
 130 135 140  
 Ala Ile Ile Ser Cys Leu Leu Trp Gly Ile Thr Val Gly Leu Thr Val  
 145 150 155 160  
 His Leu Leu Lys Lys Lys Leu Leu Ile Gln Asn Gly Pro Ala Asn Val  
 165 170 175  
 Cys Ile Ser Phe Ser Ile Cys His Thr Phe Arg Trp His Glu Ala Met  
 180 185 190  
 Phe Leu Leu Glu Phe Leu Leu Pro Leu Gly Ile Ile Leu Phe Cys Ser  
 195 200 205  
 Ala Arg Ile Ile Trp Ser Leu Arg Gln Arg Gln Met Asp Arg His Ala  
 210 215 220  
 Lys Ile Lys Arg Ala Ile Thr Phe Ile Met Val Val Ala Ile Val Phe  
 225 230 235 240  
 Val Ile Cys Phe Leu Pro Ser Val Val Val Arg Ile Arg Ile Phe Trp  
 245 250 255  
 Leu Leu His Thr Ser Gly Thr Gln Asn Cys Glu Val Tyr Arg Ser Val  
 260 265 270  
 Asp Leu Ala Phe Phe Ile Thr Leu Ser Phe Thr Tyr Met Asn Ser Met  
 275 280 285  
 Leu Asp Pro Val Val Tyr Tyr Phe Ser Ser Pro Ser Phe Pro Asn Phe  
 290 295 300  
 Phe Ser Thr Leu Ile Asn Arg Cys Leu Gln Arg Lys Met Thr Gly Glu  
 305 310 315 320  
 Pro Asp Asn Asn Arg Ser Thr Ser Val Glu Leu Thr Gly Asp Pro Asn  
 325 330 335  
 Lys Thr Arg Gly Ala Pro Glu Ala Leu Met Ala Asn Ser Gly Glu Pro  
 340 345 350  
 Trp Ser Pro Ser Tyr Leu Gly Pro Thr Ser Asn Asn His Ser Lys Lys  
 355 360 365  
 Gly His Cys His Gln Glu Pro Ala Ser Leu Glu Lys Gln Leu Gly Cys  
 370 375 380  
 Cys Ile Glu  
 385

<210> 3  
 <211> 27  
 <212> DNA  
 <213> artificial sequence

<220>  
 <223> forward primer

<400> 3  
 gagtaaagct tctaggcatc tgaaact

<210> 4  
 <211> 20  
 <212> DNA  
 <213> artificial sequence

<220>  
 <223> reverse primer

<400> 4  
 cgcctacaat ttgcccatct

27

20

- 3 -

<210> 5  
<211> 26  
<212> DNA  
<213> artificial sequence  
  
<220>  
<223> probe  
  
<400> 5  
cttcatctct gacgctcgca ggactg

26